FIGURE 1

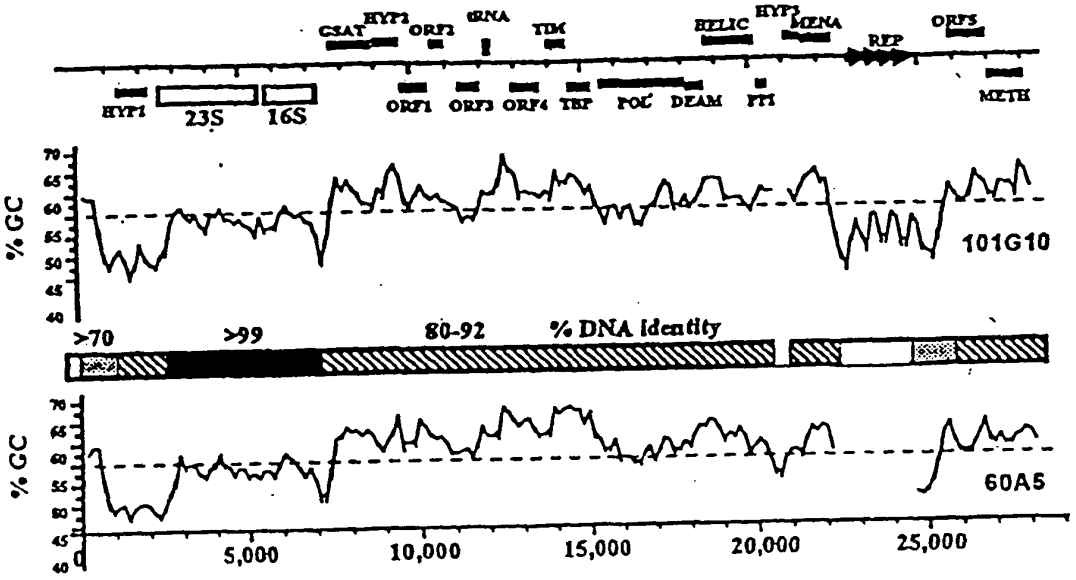
HYP1
23S
16S
ORF1
ORF3
ORF4
TBP
POL
DEAM
PT1
METH
% GC
101G10
>70
>99
80-92
% DNA identity
60A5
5,000
10,000
15,000
20,000
25,000

Figure 2

SEQ ID NO.	Gene	Strain	TATA Box	Coding Start	TATA to Start (bp)
81	Hypoth 03	A	AAGCTAGACT **TTTAAT** TGGG ATCCGGCGGG GCGGCGCATG	---------- ----------	25
82		B	AAGCTAAACT **TTTAAT** TGGG ATCCGGCGAG CCGGCGCGTG	---------- ----------	
83	Hypoth 02	A	GGAAACTTTG **ATTATA** CGGG CGTGCTGCCC CGGGGCCCAT G---------	----------	26
84		B	GGAAACTTTG **ATTATA** CGGG CGTACATTCC CGGGGCCCAT G---------	----------	
85	ORF 02	A	AAGGCAAGGT **AATAAT** AGCC TGCCGTCTGT AACGGCCGTA TG---------	----------	27
86		B	ACGGCAAGGT **AATAAT** AGCC TGCCGTCCGT ACCTGCCGTA TG---------	----------	
87	ORF 03	A	CATGGAACTA **GATATT** AACC GGTTCCGCGG ATCCCATGCA TG---------	----------	27
88		B	CATGGAACTA **GATAAT** AACC GGTCCCGCGG GTACAATGCA TG---------	----------	
89	PPI	A	ATACCGAGAA **GTTATA** GCAG GGTATGGAAT GTGCGCGCGC ATG---------	----------	28
90		B	AGCACGACAA **GTTATA** GCAG GGTACAAAGG AGCAGCGCAC ATG---------	----------	
91	GSAT	A	ATCCGCCCTG **ATTAAA** TTAT GGGGGGAGCG GCCTGCTGCC GTG---------	----------	28
92		B	ATCCGGCCTC **ATTAAA** TTAC GGGGGGTACA ACCTGCTGCC GTG---------	----------	
93	ORF 05	A	CCTTCATACA **CATAAA** TCCC GCTTGGATGT GCGGCTGCGC ATG---------	----------	28
94		B	ACTTCATACA **CATAAA** TCCC GCCTGAACGG TCGTCCGCGC ATG---------	----------	
95	deaminase	A	.GGCATATAC **CATAAT** ATGC CGGGCGGTGG CACCATGGCC GTTG-------	----------	29
96		B	CCGCATATAC **CATAAT** ATGC CGGGCGGGGG CAGGCTGCCC .GTG-------	----------	
97	RNA helic	A	TGTACGAAAC **CATAAA** ACAA CAGGCCGCGT CAGGGCCGCG CGTG-------	----------	29
98		B	GGGTAGAAAC **CATAAA** ACAA CAGGCCGCGG CAGGGCG.CG CGTG-------	----------	
99	ORF 06	A	..ACACGCAG **TATAAA** CGGG GGCCCGGGCG GCGCGTATCA CATG-------	----------	29
100		B	ATACACGTGG **TATAAA** CAGA GG.CCGGACG GCGCGGACCA CATG-------	----------	
101	tRNA-tyr	A	GCGATAGTTA **TTTAAA** ACTA GGATGCCGAT CACGGATCGT CCCA-------	----------	29
102		B	GCGATAGTTA **TTTAAA** ACTA GGATGCCGGG CACCCGTCGT CCCA-------	----------	
103	TBP	A	CCGGGCCCCG **GTTAAA** ATAG CG.CACGGGC GGATCCTGAC CAATG------	----------	30
104		B	CCGGGCCCCG **GTTAAA** ATAG AGTGCGGCCG GGCACCGGAT CAATG------	----------	
105	TIM	A	GCGTCGATAG **AATAAA** TACG CGCAGGGGGC CCCGTGGCGC GATCGCCCGT G---------		36
106		B	GCGTCGATAG **AATAAA** TACG CGC.GGGGCC GCGGTGC... GATCGCCCGT G---------		
107	Hypoth 01	A	ATTTCAACTA **CATAAA** TGCC TAGTTACGCA GAAATAGCAA ACGACGTACT TCGACTAATG		45
108		B	ACTTCAACTA **CATAAA** TGCC TAGCTACGCA GAAATATCAA ACAAAGTACT TCGACTAATG		
109	ORF 01	A	ACGGCAGGCT **ATTATT** ACCT TGCCTTGCGT TGTA //..G CGGGGTGCGG CAGGGGATG		52
110		B	ACGGCAGGCT **ATTATT** ACCT TGCCGTGTG. TACA //..G AGGGGGCCTG CCGGGAGTG		
111	Methylase	A	CTACAACGAT **TTTAAG** TCGG CGCCGGGGCA GCCG.//..G ATGTGGGGCA GGCAACATG		104
112		B	CTACAAAGAT **TTTAAG** ACGG CGCGGGTGCC GCGG.//..T GGCACGGGGG CCTATCTTG		
113	16S RNA	A	TCGGCGATGG **TTTATA** TGCC CATGGACGGG CCGATCCGAT CGTACGTGAC GC.//..AAT		220
114		B	CCGGCGATGG **TTTATA** TGCC CATGGACAAG GCGATCCGAT CGTACGTGAC GC.//..AAT		
	Archaeal promoter consensus		**YTTAWA**		

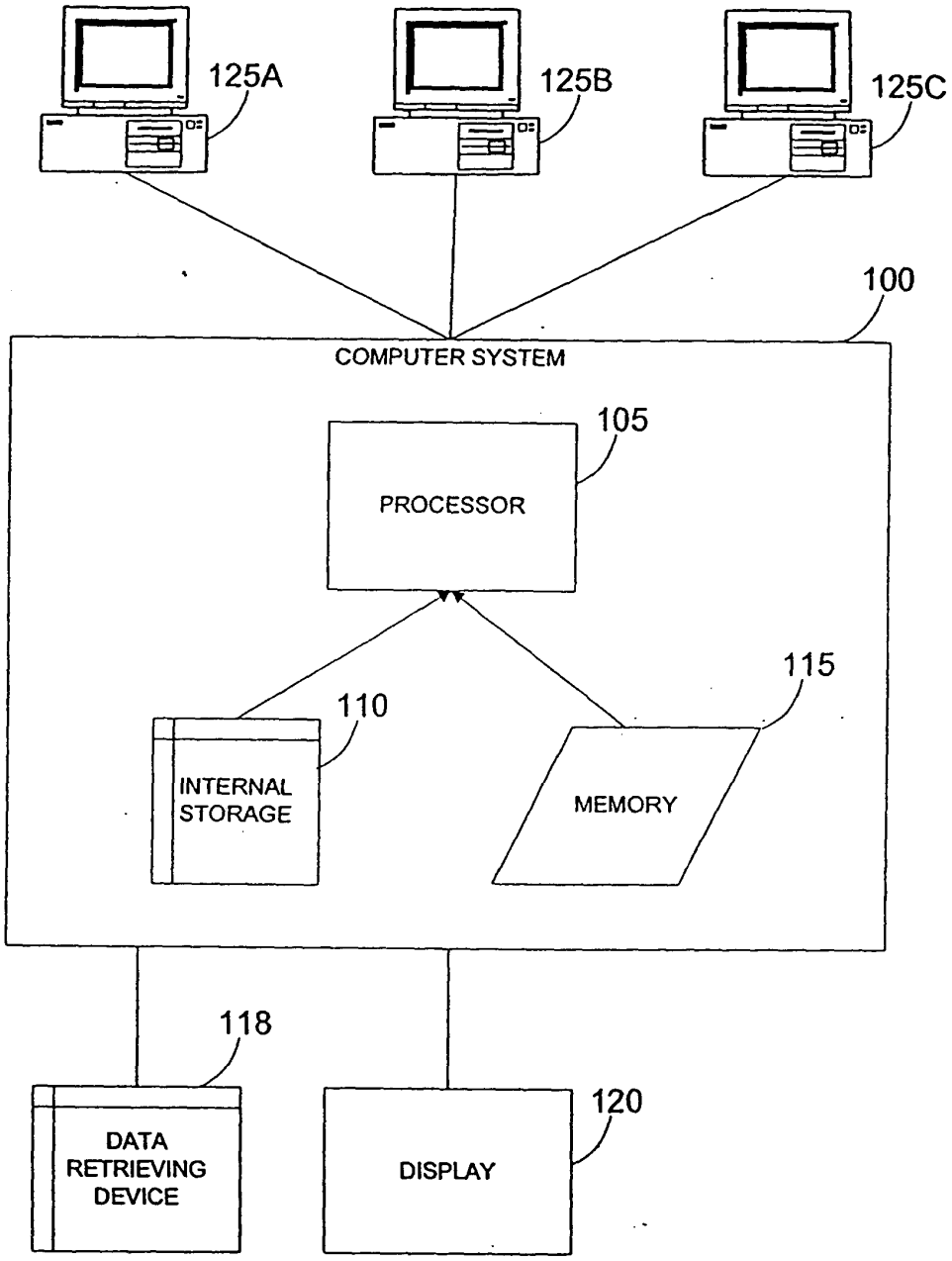
125A
125B
125C
100
COMPUTER SYSTEM
105
PROCESSOR
115
110
INTERNAL STORAGE
MEMORY
118
DATA RETRIEVING DEVICE
120
DISPLAY

FIGURE 3

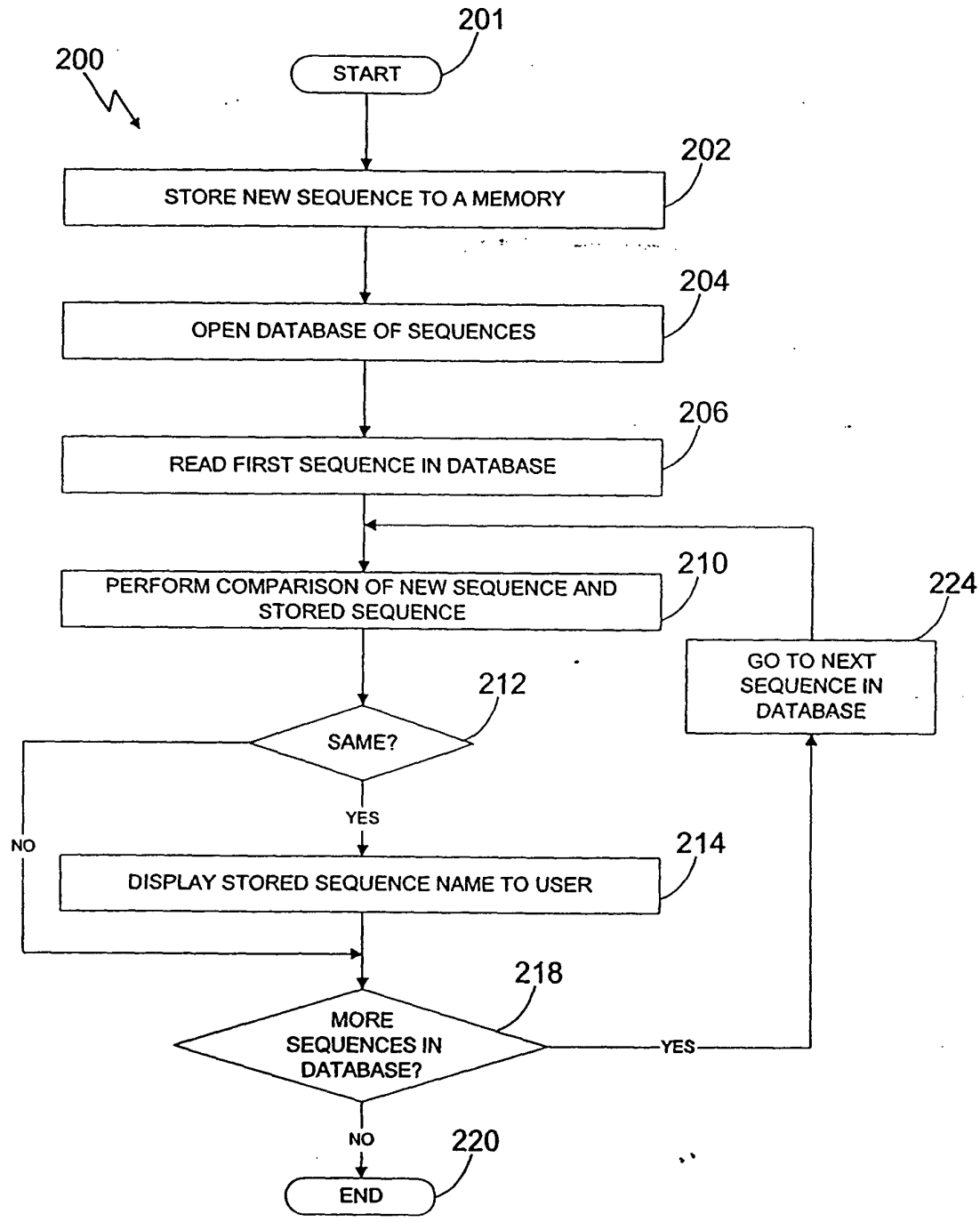
200
201
START
202
STORE NEW SEQUENCE TO A MEMORY
204
OPEN DATABASE OF SEQUENCES
206
READ FIRST SEQUENCE IN DATABASE
210
PERFORM COMPARISON OF NEW SEQUENCE AND STORED SEQUENCE
212
SAME?
YES
NO
214
DISPLAY STORED SEQUENCE NAME TO USER
218
MORE SEQUENCES IN DATABASE?
YES
NO
220
END
224
GO TO NEXT SEQUENCE IN DATABASE

FIGURE 4

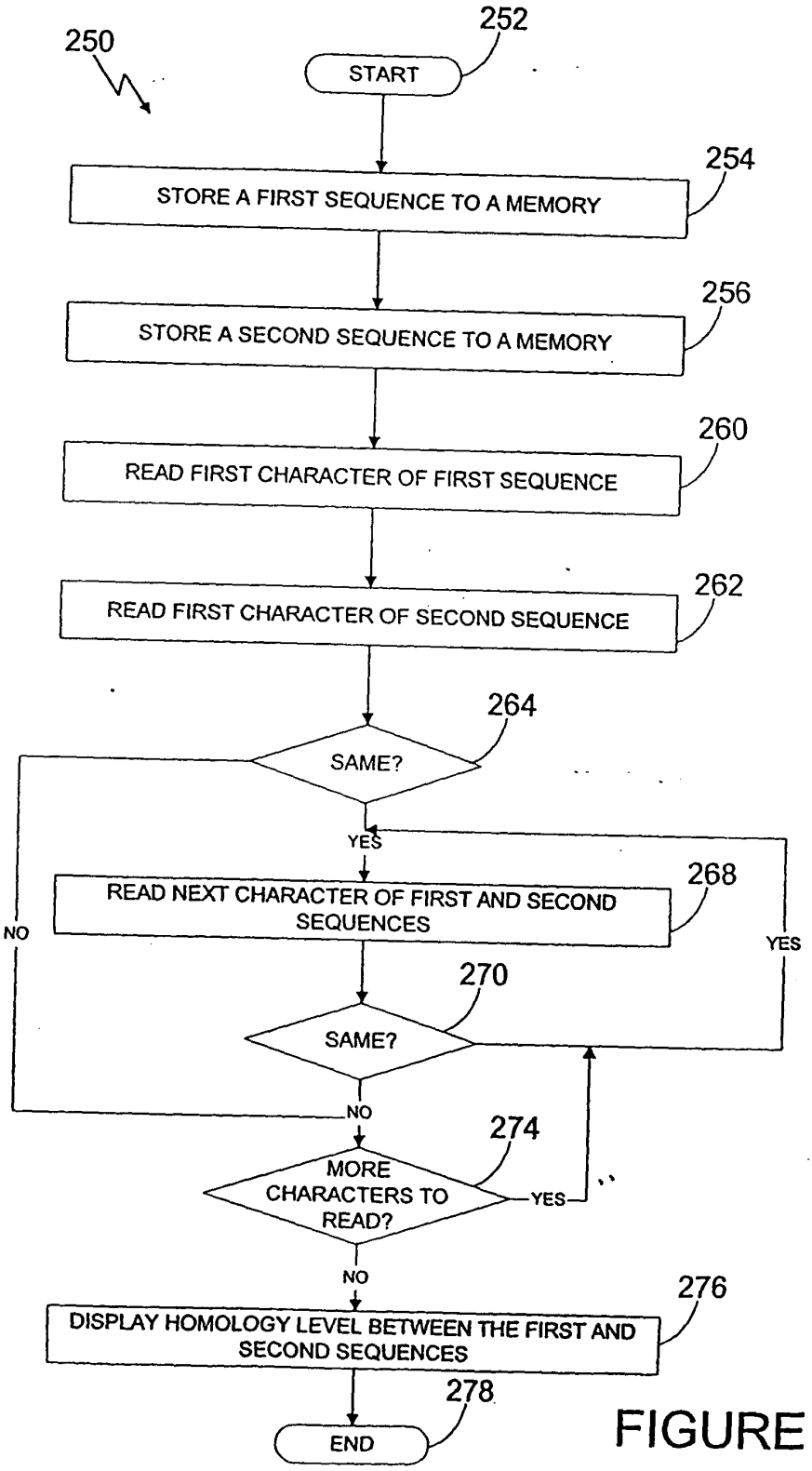
250
252
START
254
STORE A FIRST SEQUENCE TO A MEMORY
256
STORE A SECOND SEQUENCE TO A MEMORY
260
READ FIRST CHARACTER OF FIRST SEQUENCE
262
READ FIRST CHARACTER OF SECOND SEQUENCE
264
SAME?
YES
NO
268
READ NEXT CHARACTER OF FIRST AND SECOND SEQUENCES
YES
270
SAME?
NO
274
MORE CHARACTERS TO READ?
YES
NO
276
DISPLAY HOMOLOGY LEVEL BETWEEN THE FIRST AND SECOND SEQUENCES
278
END

FIGURE 5

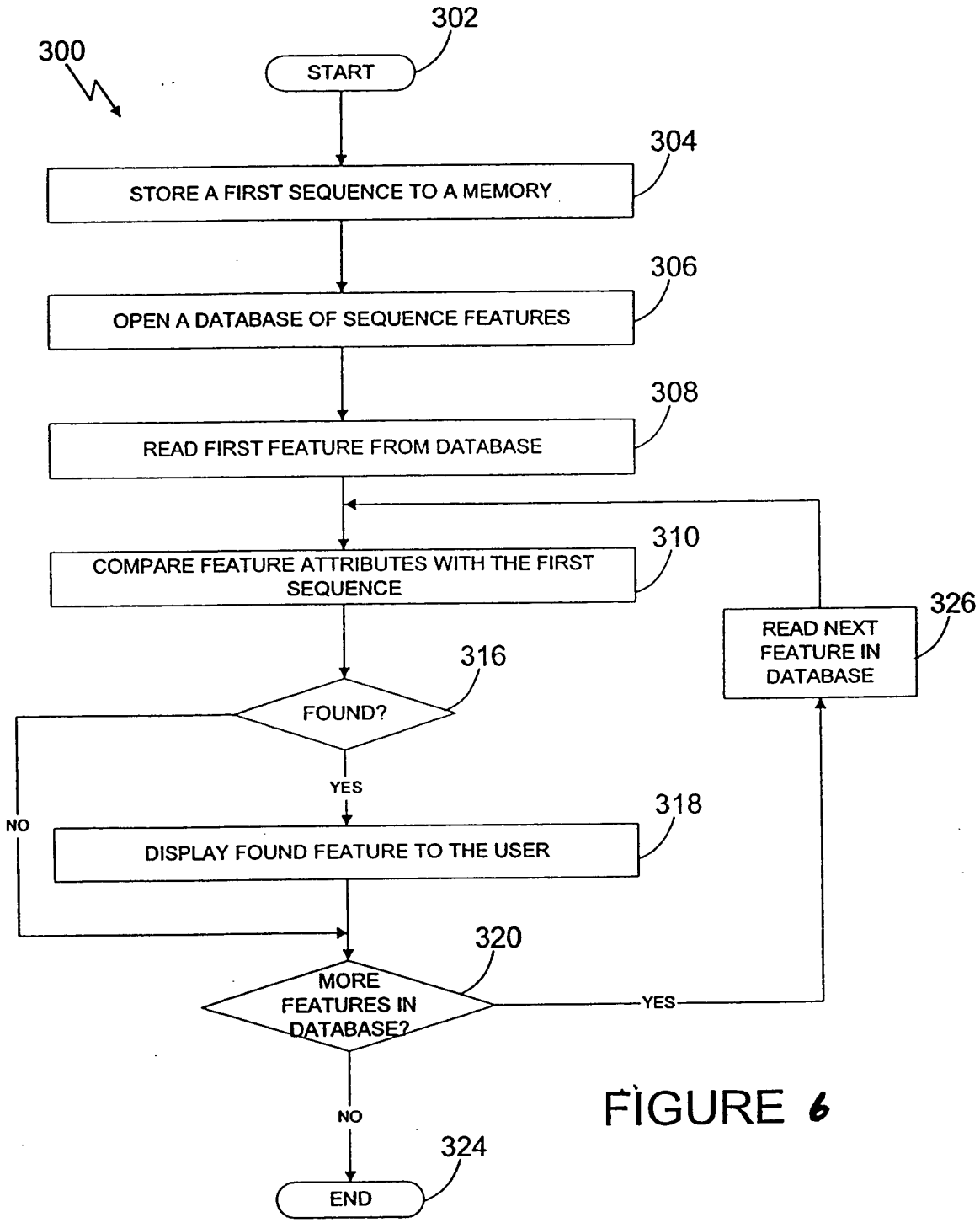
300
302
START
304
STORE A FIRST SEQUENCE TO A MEMORY
306
OPEN A DATABASE OF SEQUENCE FEATURES
308
READ FIRST FEATURE FROM DATABASE
310
COMPARE FEATURE ATTRIBUTES WITH THE FIRST SEQUENCE
316
FOUND?
YES
NO
318
DISPLAY FOUND FEATURE TO THE USER
320
MORE FEATURES IN DATABASE?
YES
NO
324
END
326
READ NEXT FEATURE IN DATABASE

FIGURE 6